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b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:20.

REMARKS

Claims 1-19 and 22-45 were pending in the application. Claims 1-19 and 22-26 have been cancelled, without prejudice, and new claims 46-49 have been added. Accordingly, after the amendments presented herein have been entered, claims 27-49 will remain pending. For the Examiner's convenience all of the pending claims are set forth herein in Appendix A.

Support for the newly added claims can be found throughout the specification and claims as originally filed. Specifically, support for new claims 46, 47, 48 and 49 can be found in claims 27, 28, 37 and 38 as originally filed, respectively. Further support for newly added claims 46-49 can be found at page 11, lines 10-24, and page 8, lines 35-38 of the specification.

No new matter has been added. Any cancellation of the claims should in no way be construed as an acquiescence to any of the Examiner's rejections and was done solely to expedite the prosecution of the application. Applicant reserves the right to pursue the claims as originally filed in this or a separate application(s).

Withdrawal From Consideration of Claims 28, 30, 32-36, 38, 40, and 42-45 As Being Directed to a Non-Elected Invention

The Examiner has withdrawn claims 28, 30, 38, 40, and claims 32-36 and 42-45 in so far as they depend from any of claims 28, 30, 38, and 40, as being directed toward an invention that is independent or distinct from the invention originally claimed.

Applicant traverses the withdrawal from consideration of these claims for the following reasons. The polypeptide that the Examiner believes is independent from the invention that was originally claimed (SEQ ID NO:20) is a *splice varian*t of claimed polypeptide (SEQ ID NO:5). Both SEQ ID NO:20 and SEQ ID NO:5 are human capsaicin/vanilloid receptor polypeptides and share a high degree of sequence identity. The two polypeptides are identical with the exception of 164 residues that are deleted in the spice variant (see Figure 17 of the instant application for a



sequence alignment) and share the same structural features. Accordingly, the two polypeptides share a common utility which is based upon shared structural and functional features and, thus, have a unity of invention. Moreover, a search of the full length polypeptide would by default also search the splice variant and, thus, no additional searches that would pose undue burden on the Examiner would be necessary. Therefore, SEQ ID NO:20 is not directed toward an invention that is distinct from the invention originally claimed, and Applicant respectfully requests that the claims directed toward SEQ ID NO:20 be considered and examined by the Examiner.

Rejection of Claims 31-36 and 41-45 Under 35 U.S. C. § 112, First Paragraph

The Examiner has rejected claims 31-36 and 41-45, under 35 U.S.C. § 112, first paragraph because, "the specification, while being enabling for the practice of a method of identifying a ligand which binds to a receptor protein comprising the amino acid sequence presented in SEQ ID NO:5 of the instant specification, does not reasonably provide enablement for the practice of a binding assay which employs a protein having anything less than the entire amino acid sequence presented in SEQ ID NO:5" (Emphasis added). The Examiner is further of the opinion that

[t]he instant specification specifically identifies notable structural features of a protein of the instant invention. It neither provides the identification of the expendable residues in SEQ ID NO:5 nor even a single working example of a functional protein lacking its entire native amino acid sequence.

Applicant traverses this rejection for the following reasons. As indicated in Applicant's previous reply, the teachings in Applicant's specification, and the knowledge generally available in the art at the time of filing would allow a skilled artisan to practice the claimed methods using only routine experimentation.

Contrary to the Examiner's assertions, Applicant has taught in the instant specification which regions of the VR-2 molecules are important for activity and, thus, which regions of the molecule would respond in a binding assay in a manner which is representative of the native protein. Specifically, as taught in the specification (at, for example, page 10, lines 1-35; page 66, lines 30-34; and page 67, lines 1-11), the VR-2 polypeptide contains ankyrin repeats, transmembrane domains, and at least one proline rich domain, all characteristic and necessary for the function of the Capsaicin/Vanilloid family of receptors. Based on these teachings in Applicant's specification, the skilled artisan would be equipped to use a fragment containing one or more of these functional

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domains to identify compounds that bind to a domain and modulate an activity of the Capsaicin/Vanilloid receptor. Compounds identified in such a manner would be of practical value, e.g., they could be used as antagonists of a Capsaicin/Vanilloid receptor. For example, as taught in Applicant's specification a fragment of a VR-2 polypeptide containing the proline rich domain may be used by the skilled artisan to identify compounds capable of binding the proline rich domain and disrupting interactions with SH3 domain-containing proteins that act downstream of the VR-2 receptor in a pain signaling pathway. Such a compound would be expected to inhibit the function of the VR-2 polypeptide by disrupting the VR-2 signaling pathway.

Further, contrary to the Examiner's assertion, Applicant does disclose a working example of a fragment of SEQ ID NO:5. SEQ ID NO:20 is a splice variant of SEQ ID NO:5 that is identical in sequence to SEQ ID NO:5 with the exception of a 134 residue deletion from residue 529-663 (see the sequence alignment presented in Figure 17). Moreover, in Example 5 Applicant discloses specific fragments of SEQ ID NO:5 that were used to generate antibodies against human VR2 (see SEQ ID NOs:13, 14 and 15 at page 70 of the specification).

The Examiner further states that, "Applicant has cited a plurality of patent documents in traversal of this rejection. Applicant is advised that none of the patents cited were available at the time the instant application was filed." Applicant respectfully submits that, although the patents submitted were not *issued* at the time Applicant filed the instant application, the patents were submitted prior to Applicant's filing date and, thus, *prove that the methods disclosed therein were common and well known to those of ordinary skill in the art at the time of Applicant's filing.*

With respect to the newly added claims 46-49 which are directed to methods of identifying compounds that modulate polypeptides that are 95% identical to the hVR2 molecules, Applicant would like to point the Examiner's attention to Example 14 Revised Interim Written Description Guidelines Training Materials. Example 14 provides that a claim directed to variants of a protein having SEQ ID NO:3 "that are at least 95% identical to SEQ ID NO:3 and catalyze the reaction of A→B" with an accompanying specification that discloses a single species falling within the claimed genus, satisfies the requirements of 35 U.S.C. §112, first paragraph for written description. The rationale behind the foregoing conclusion, as presented by the Written Description Guidelines, is that "[t]he single species disclosed is representative of the genus because all members have at least 95% structural identity with the reference compound and because of the presence of an assay which Applicant provided for identifying all of the at least 95% identical variants of SEQ ID NO:3 which are capable of the specified catalytic activity." The Guidelines also provide that "[t]he procedures

for making variants of SEQ ID NO:3 are conventional in the art and an assay is described which will identify other proteins having the claimed catalytic activity. Moreover, procedures for making variants of SEQ ID NO:3 which have 95% identity to SEQ ID NO:3 and retain its activity are conventional in the art."

Similarly, in the present case, the claims are directed to methods which use isolated nucleic acid molecules encoding hVR-2 polypeptides comprising an amino acid sequence that is at least 95% identical to the amino acid sequence shown in SEQ ID NOs:5 and 20, wherein the polypeptide is capable of modulating membrane excitability. Furthermore, Applicant has disclosed in the instant specification assays for identifying all of the at least 95% identical variants of SEQ ID NO:5 and 20 which encode polypeptides capable of modulating membrane excitability (see, for example, the patch-clamp methods taught by the Applicant in Example 4). Modulation of membrane excitability is readily testable by one of skill in the art by the methods described in the instant specification and by methods well-known in the relevant art. Accordingly, it would require only routine experimentation on the part of one of skill in the art to mutate the VR-2 molecules of the invention and test them for the ability to modulate membrane excitability as described in the specification.

Based on the foregoing teachings in Applicant's specification and the knowledge generally available in the art at the time of filing, Applicant respectfully submits that the skilled artisan would be able to make and use the claimed invention using only routine experimentation. Accordingly, Applicant respectfully requests that the Examiner reconsider and withdraw the foregoing rejection.

Rejection of Claim 42 Under 35 U.S. C. § 112, First Paragraph

The Examiner has rejected claim 42 under 35 U.S.C. § 112, first paragraph because, "[i]t was well know in the art prior to the time of the instant application that the yeast two-hybrid system can only employ small soluble proteins as shown in Figure 1 of the Chien *et al.* publication." The Examiner is further of the opinion that

[o]ne of ordinary skill in the art of molecular biology would immediately recognize that a yeast two-hybrid system which employed all of the amino acid sequence of SEQ ID NO:5 would be inoperative because the presence of the six transmembrane domains within that sequence (Figure 1B of Julius *et al.* Pat. No. 6,335,180). In so far as this claim encompasses a system employing only a soluble portion of the amino acid sequence of SEQ ID NO:5, the instant specification does not disclose a practical utility which is to be realized from the identification of a protein which bind[s] to a portion of that amino acid sequence.

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Applicant traverses the forgoing rejection for the following reasons. Contrary to the Examiner's assertions, employing fragments of SEQ ID NO:5 in yeast two hybrid assays would be useful in finding modulators that disrupt pain signaling mechanisms. One of ordinary skill in the art would immediately recognize the potential applications of using fragments of a transmembrane protein in screening assays to identify compounds that are capable of binding to an insoluble transmembrane protein. Identification of a compound that binds to a fragment of a transmembrane protein is useful in the modulation of the activity of the protein. For example, a particularly useful application would be the identification of a compound that is capable of binding to an extracellular region of the transmembrane protein and either blocks natural ligand binding, or itself modulates hVR-2 activity in some other manner. Applicant's specification discloses the presence of proline rich domains in hVR-2 polypeptides. Proline rich domains are known to interact with SH3 domains in proteins that act upstream or downstream of hVR-2 in a pain signaling pathway and, thus, the proline rich domains of VR-2 are useful in screening for modulators that disrupt the pain signaling mechanism. Moreover, Applicant's specification provides a hydrophobicity plot for hVR-2 that an ordinary skilled artisan would be able to use to identify those regions of the protein that are on the cell surface. The use of these portions of the protein would allow for the identification of compounds that themselves modulate the activity of the receptor, or through steric effects, abolish the ability of the receptor to bind to other ligands.

Based on the foregoing teachings in Applicant's specification, and the knowledge generally available to one skilled in the art at the time of filing, it is obvious that the ordinary skilled artisan would realize the applications of using fragments of hVR-2 in a two-hybrid system, and would further be able to make and use the claimed invention using only routine experimentation. Accordingly, Applicant respectfully requests that the Examiner reconsider and withdraw the foregoing rejection.

Rejection of Claims 27, 29, 31-34, 36, 37, 39 41, and 43-45 under 35 U.S.C. 102 (e)

The Examiner has rejected claims 27, 29, 31-34, 36, 37, 39 41, and 43-45, under 35 U.S.C. § 102(e) as being anticipated by Julius *et al.* (United States Patent No. 6,335,180 B1). In particular, the Examiner is of the opinion that "[t]he amino acid sequence presented in SEQ ID

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NO:5 of the instant application is identical to the amino acid sequence presented in SEQ ID NO:36 of the Julius *et al.* patent."

Applicant respectfully traverses the aforementioned rejection for the following reasons. As evidenced by copies of U.S. Application Serial No: 08/915,461, Provisional Application Serial No: 60/072,151 and PCT application Serial No. PCT/US98/17466 (submitted herewith as Appendices B, C, and D, respectively) to which Julius *et al.* claim priority, *SEQ ID NO:36 is not disclosed in any of these applications*. Accordingly, the 35 U.S.C. § 102(e) date that Julius *et al.* are entitled to with respect to SEQ ID NO:36, is *January 22, 1999*, the filing date of the Julius *et al.* patent (6,335,180 B1). Moreover, Julius *et al.* disclose *but do not claim* the amino acid sequence set forth in SEQ ID NO:36.

Applicant submits herewith a declaration under 37 CFR §1.131 which indicates that Applicant has completed the invention as described and claimed in the above-referenced patent application in this country *prior to January 22, 1999*. Accordingly, Applicant respectfully submits that the invention disclosed in the present patent application was reduced to practice by the inventor prior to the effective date of the Julius *et al.* reference. As such, the Julius *et al.* reference is not available as prior art against the present invention under 35 U.S.C. 102§(e), and Applicant respectfully requests that the Examiner reconsider and withdraw this rejection.

Rejection of Claim 35 under 35 U.S.C. 103 (a)

The Examiner has rejected claim 35 under 35 U.S.C. § 103(a) as being unpatentable over Julius *et al.* Specifically, the Examiner believes

[b]ecause the Julius *et al.* patent disclosed the fact that the receptor described therein was naturally expressed in neuronal tissue an artisan would have found it *prima facie* obvious to have expressed that protein recombinantly in a neuronal cell line to obtain a more authentic response by that receptor to a test compound.

Applicant respectfully submits that, in view of the declaration under 37 CFR §1.131 submitted herewith, the aforementioned rejection is rendered moot. Accordingly, Applicant respectfully requests that the Examiner reconsider and withdraw this rejection.

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Rejection of Claim 42 under 35 U.S.C. 103 (a)

The Examiner has rejected claim 42 under 35 U.S.C. § 103(a) as being unpatentable over Julius *et al.* in view of Chien *et al.* Specifically, the Examiner believes that

[t]o have incorporated portions of the capsaicin receptor of Julius *et al.* into the yeast two hybrid system of Chien *et al.* to identify proteins with might interact therewith would have been *prima facie* obvious to one of ordinary skill in the art.

Applicant respectfully submits that, in view of the declaration under 37 CFR §1.131 submitted herewith, the Julius *et al.* patent is not available as prior art against the instant application. The Chien *et al.* publication, by itself, is not sufficient to render claim 42 obvious to one of ordinary skill in the art. Accordingly, Applicant respectfully requests that the Examiner reconsider and withdraw this rejection.

SUMMARY

If a telephone conversation with Applicant's attorney would expedite the prosecution of the above-identified application, the Examiner is urged to call the undersigned at (617) 227-7400.

Respectfully submitted,

LAHIVE & COCKFIELD, LLP

Maria Laccotripe Zacharakis, Ph.D.

Attorney for Applicant

Limited Recognition Under 37 CFR §10.9(b)

28 State Street Boston, MA 02109

Telephone: (617) 227-7400 Facsimile: (617) 742-4214

Dated: September 25, 2002

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Appendix A

27. A method for identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:5, the method comprising:

- a) contacting a cell expressing the polypeptide with a test compound under conditions suitable for binding; and
- b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:5.
- 28. A method for identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:20, the method comprising:
 - a) contacting a cell expressing the polypeptide with a test compound under conditions suitable for binding; and
 - b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:20.
- 29. A method for identifying a compound which binds to a polypeptide consisting of the amino acid sequence of SEQ ID NO:5, the method comprising:
 - a) contacting a cell expressing the polypeptide with a test compound under conditions suitable for binding; and
 - b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide consisting of the amino acid sequence of SEQ ID NO:5.
- 30. A method for identifying a compound which binds to a polypeptide consisting of the amino acid sequence of SEQ ID NO:20, the method comprising:
 - a) contacting a cell expressing the polypeptide with a test compound under conditions suitable for binding; and

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b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide consisting of the amino acid sequence of SEQ ID NO:20.

- 31. A method for identifying a compound which binds to a polypeptide comprising at least 15 contiguous amino acids of SEQ ID NO:5, the method comprising:
 - a) contacting a cell expressing the polypeptide with a test compound under conditions suitable binding; and
 - b) determining whether the test compound binds to said polypeptide, thereby identifying a compound which binds to a polypeptide comprising at least 15 contiguous amino acids of SEQ ID NO:5.
- 32. The method of any one of claims 27-31, wherein binding of the test compound to the polypeptide is detected by the use of an assay for a hVR-2 activity.
- 33. The method of claim 32, wherein said hVR-2 activity is modulation of membrane depolarization.
- 34. The method of claim 32, wherein said hVR-2 activity is modulation of intracellular calcium levels.
- 35. The method of any one of claims 27-31, wherein said cell expressing said polypeptide is a neuronal cell.
- 36. The method of any one of claims 27-31, wherein said compound modulates the activity of said polypeptide.
- 37. A method for identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:5, the method comprising:
 - a) contacting a sample comprising the polypeptide with a test compound under conditions suitable for binding; and

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b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:5.

- 38. A method for identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:20, the method comprising:
 - a) contacting a sample comprising the polypeptide with a test compound under conditions suitable for binding; and
 - b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:20.
- 39. A method for identifying a compound which binds to a polypeptide consisting of the amino acid sequence of SEQ ID NO:5, the method comprising:
 - a) contacting a sample comprising the polypeptide with a test compound under conditions suitable for binding; and
 - b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide consisting of the amino acid sequence of SEQ ID NO:5.
- 40. A method for identifying a compound which binds to a polypeptide consisting of the amino acid sequence of SEQ ID NO:20, the method comprising:
 - a) contacting a sample comprising the polypeptide with a test compound under conditions suitable for binding; and
 - b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide consisting of the amino acid sequence of SEQ ID NO:20.
- 41. A method for identifying a compound which binds to a polypeptide comprising at least 15 contiguous amino acids of SEQ ID NO:5, the method comprising:
 - a) contacting a sample comprising the polypeptide with a test compound under conditions suitable for binding; and

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- b) determining whether the test compound binds to said polypeptide, thereby identifying a compound which binds to a polypeptide comprising at least 15 contiguous amino acids of SEQ ID NO:5.
- 42. The method of any one of claims 27-31 or 37-41, wherein binding of said test compound to said polypeptide is detected by the use of a yeast two-hybrid assay.
- 43. The method of any one of claims 37-41, wherein binding of said test compound to said polypeptide is detected by the use of a direct binding assay.
- 44. The method of any one of claims 37-41, wherein binding of said test compound to said polypeptide is detected by the use of a competition binding assay.
- 45. The method of any one of claims 37-41, wherein said test compound modulates the activity of said polypeptide.
- 46. A method for identifying a compound which binds to a polypeptide that is 95% identical to the amino acid sequence of SEQ ID NO:5 and is capable of modulating membrane excitability in a cell, the method comprising:
 - a) contacting a cell expressing the polypeptide with a test compound under conditions suitable for binding; and
 - b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:5.
- 47. A method for identifying a compound which binds to a polypeptide that is 95% identical to the amino acid sequence of SEQ ID NO:20 and is capable of modulating membrane excitability in a cell, the method comprising:
 - a) contacting a cell expressing the polypeptide with a test compound under conditions suitable for binding; and

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b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:20.

- 48. A method for identifying a compound which binds to a polypeptide that is 95% identical to the amino acid sequence of SEQ ID NO:5 and is capable of modulating membrane excitability in a cell, the method comprising:
 - a) contacting the polypeptide with a test compound under conditions suitable for binding; and
 - b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:5.
- 49. A method for identifying a compound which binds to a polypeptide that is 95% identical to the amino acid sequence of SEQ ID NO:20 and is capable of modulating membrane excitability in a cell, the method comprising:
 - a) contacting the polypeptide with a test compound under conditions suitable for binding; and
 - b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:20.

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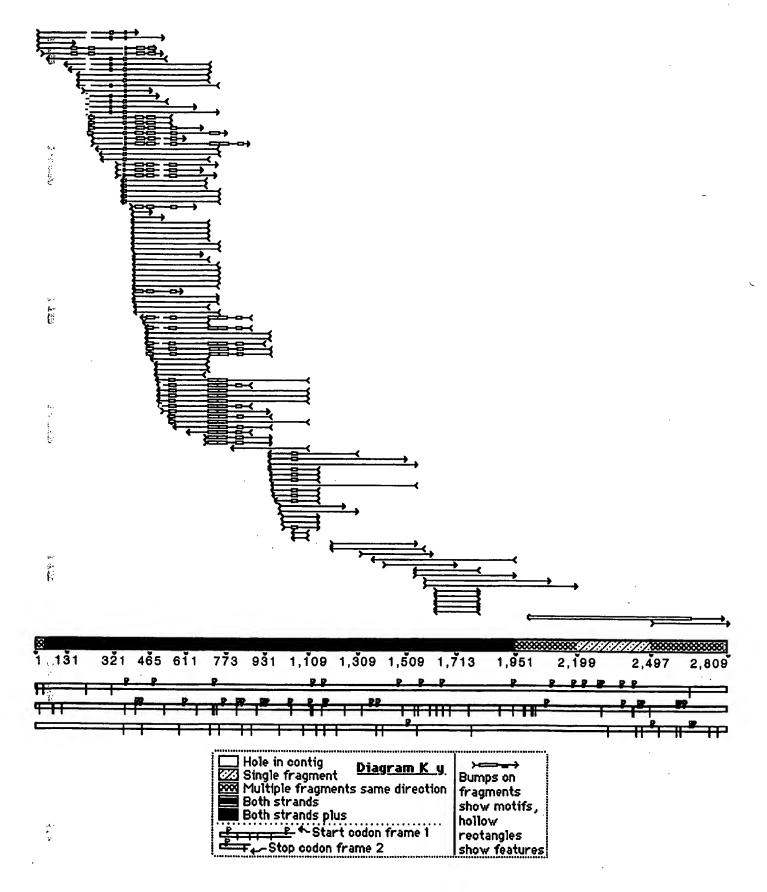


Exhibit B

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# flbx2le11x21a1 #16 ACCGACGCGC AGCT:GGAGG AAGACAGGAC CCTTGACATC TCCATCTGCA CAGAGGTCCT GGCTGGACCG AGCAGCCTCC TCCTCCTAGG
🛍 flbx21e11r21g2 #13 accgacongc agntoggagg aagacaggac cettgaente tecatetgea cagaggteet ggntggaeeg agcageetee tecteetagg
4 Genbank H20.. >#1>
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                                                                                                                    G
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                                                                           AGAGGTCCT GGCTGGACAT :GCAGCCTCC TCCTCC
                                                                                                                   G
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T D A Q L G G R Q D P . H L H L H R G P G W T E Q P P P P R

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	flhxc21ellz2					T AGGTTGGAG					•
	filhXc21e11z1	#361	ATGACCTCAC	CCTNCAACTO	TTCAGTTTT	T AAGNTGGAG	A CATTATATG	G AGGNCCAAA	A NATGGCTCTN	AGGCGGACA	A ANGAAA:CTT
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4	flhXc21e11g2	#248	ATGACCTCAC	CCTCCAGCTC	TCCAGTTTT	AGGTTGGAG	A CATTAGATG	G ACCCCAACA	GATGGCTCTG	AGGCGGACA	G AGGAAAGCTG G AGGAAAGCTG
i	a flhxc21e11g1	#230	ATGACCTCAC	CCTCCAGCTC	ተርርል በጥጥጥጥ(AGGTTGGAG	. Chundalo	C ACCCAAGA	GATGGCTCTG	AGGCGGACA	G AGGAAAGCTG G AGGAAAGCTG
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拒	flhx21e11r20g	2 #22	ATGACCTCAC	CCTCCAGCTC	TCCAGTTTTC	ACCOMOCCCA	CATTAGATGG	AGGCCAAGAA	GATGGCTCTG	AGGCGGACAG	AGGAAAGCTG
福	flhx21e11r22a	2 #22	ATGACCTCAC ATGACCTCAC	27つの私のつでつつ	TCCAGTTTTC	AGGTTGGGGA	CATTAGATGG	AGGCCAAGAA	GATGGCTCTG	AGGCGGACAG	AGGAAAGCTG
1	f1hx21e11r22a	1 #22	ATGACCTCAC	CCTCCAGCTC	TCCAGITITC	AGGTTGGAGA	CATTAGATGG	AGGCCAAGAA	GATGGCTCTG	AGGCGGACAG	AGGAAAGCTG
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	f1hx21e11r16								GATGGCTCTG		
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	flhX21e11rrl	>#1>							GATGGCTCTG A		
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侧	flhx21e11r17	>#1>							GATGGCTCTG /		
袒	flhX21e11r16:	>#1>							GATGGCTCTG /		
掴	flhx21e11r16_ :	*1>							GATGGCTCTG /		
個	Genbank AA7:	*#1 >									
掴	flhx21e11r22:	* 1>						Α.	GATGGCTCTG ;		
4	Genbank AA7 :	* 1>							,	GGGGACAG	AGGAAAGCTG
搁	flhX21e11r19 :	*#1>									GAAAGCTG
搁	flhx21e11r19 :	*#1 >									AAAGNTG
	Genbank All >										AAAGNTG
_											AGCTG

#361 ATGACCTCAC CCTCCAGCTC TCCAGTTTTC AGGTTGGAGA CATTAGATGG AGGCCAAGAA GATGGCTCTG AGGCGGACAG AGGAAAGCTG
M T S P S S S P V F R L E T L D G G Q E D G S E A D R G K L

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21ella Sequencher* "21ellracefinal"

162											
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	flhX21e11rrl					TCC	A: GGCGAGGN	CGGAAATTTC	NCCCNTCAGA	TAAAAGTCAC	CCTCAACTNC
	Genbank AA4						AGGGCGAGGA	CCGGAAATT	CTCAGA	TAAGAGTCAA	CCTCAACTAC
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	f1hX21e11rr1						GGGCGAGGA	CCGGAAATTN	GCCCNTCAGA	TAAGAGTCAA	CCTCAACTAC
	flhX21ellrrl							NCGGAAATTC			
個	Genbank AA8	. >#1>						CCGGAAATT		TAAGAGTCAA	
	Genbank AA2							TC		TAAGAGTCAA	
徊	jthsa103e2w1	>#1>									TAC
	0.4										

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Genbank AA8	1 #44	CGA	AAG	GGA	A C	AGGI	rgcc	AG	TC	AGCC	GGAT	CCA	AAC	CGAT	T	TGAC	CGAG	A 1	rcgg	CT	CTTC	AA	rgcg	GTC	T C	2001	agg [,]	тат	ccc	CGA	GGAT
Genbank AA2		CGA	AAG	G : A	A C	AGGT	rgcc	AG	TC	AGCC	GGAT	CCA	AAC	CGAT	T	TGAC	CGAG	A I	rcgg	CT	СТТС	AA	rgcg	GTC	T C	CCG	GGG'	TGT	CCC	: GA	GGAT
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jthsa103e2x2	>#1>															TGAC															
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	#541	CGA	AAG	GGA	A C	GGI	GCC	AG	TC.	AGCC	GGAT	CCA	AAC	CGAT	T	TGAC	CGAG.	A T	CGG	CTC	TTC	AAT	raca	GTC:	гс	CCG	3GG1	rgr	ccc	CGA	GAT
		R	K	G	T	G	A	s		Q P	D	P	N	R				D	R		P		A			R			P		
		++	٠	•		•	•	•	+	• + •	+	+•	+			++•	+•				++•						_	-			

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                    W C Y G P V R V S L Y D L A S V D S C E E N S V L E I I A P
√ frhob012c04s... ∜501 CATTGCAAGA GCCCGCACCG ACACCGAATG GTCGNTTTGG AGCCCCTGAA CAAACTGCTG C
🗖 fridod012c04s... #501 CATTGCAAGA ACCCGCACCG ACACCGAATG GTCGNTTTGG AGCCCCTGAA CAAACTGCTG CANGCGAAAT GGGATCTGCT CAT:CCCAAG
🛱 frboc12c4h3... $493 Cattgcaaga gcccgcaccg acaccgaatg gtcgttttgn agcccctgaa caaactgctg caggcgaaat gggatctgct catccccaag
4 jtbla029c10t... $247 Cattgcaaga gcccgnaccg acaccgaatg gtcgttttgg agcccctgaa caaactgctg cangcgaaat gggatctgct catnoncaag
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√ Gendank AA3... $128 CATTGCAAGA GCCCGCACCG ACACCGAATG GTCGTTTTGG AGCCCCTGAA CAAACTGCTG CAGGCGAAAT GGGATCTGCT CATCCCCAAG
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🜓 Gembank N242... #31 CATTGCAAGA GCCCGNACCG ACACCGAATG GTCGTTTTGG AGCCCCTGAA CAAACTGCTG CAGGCGAAAT GGGATCTGCT CATCCCCAAG
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                                                                                     Q A K W D L L I P K
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frhoc12c4h3... #583 TTCTTCTTAA ACTTCCTG
# jthLa029c10t.. #337 TTCTTNTTAA ACTTC
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4回 frhobl2c4c1... $261 CCTCACCTGA AAGCGGAGGT TGGAAACTCC ATGCTGCTGA CGGGCCACAT CCTTATCCTG CTAGGGGGGA TNTACCTCCT CGTGGGCCAG
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#2701	TCCAACCACA S N H		CTGGGGTCCC W G P		GGTGGCAAAT W Q I	ATATATTTC Y I F	ACTAACTCAA T N S	AAAAAAA AA K	AAAAAAAA K K K
√ frhobl2c4dl #295	to the state of th	***************************************							
#2791	AAAAAAAAA	АААААААА							

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Expires: August 5, 2003

Harry I. Moatz

Director of Enrollment and Discipline